

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:26:03 ; Search time 29.37 Seconds
(without alignments)
21.991 Million cell updates/sec

Title:	US-09-331-631A-37
Perfect score:	52

Sequence: 1 CXXXXXXXXXXXXXXCXXC 20

1 CXXXXCXXXXXXXXXXCXXXXC 20

Scoring table: BLOSUM62DX

Gapor 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	52	100.0	43	1	MTA_COLOVI	P27086 collinus vird
2	52	100.0	43	1	MTB_COLOVI	P27087 collinus vird
3	52	100.0	47	1	THN_PYRRU	P07504 pyrularia p
4	52	100.0	48	1	PIGU_HIRNI	P81499 hirudo nipp
5	52	100.0	48	1	TX26_PHONI	P29425 phoneutria
6	52	100.0	49	1	TX25_PHONI	P29424 phoneutria
7	52	100.0	55	1	ANTA_HIRME	P80302 hirudo med
8	52	100.0	55	1	M84C_DROME	O01444 drosophila
9	52	100.0	56	1	M87E_DROME	P08175 drosophila
10	52	100.0	57	1	GUAM_HIRNI	P46443 hirudo nipp
11	52	100.0	60	1	MTA_SPARU	P52727 sperus aurt
12	52	100.0	60	1	MTA_THECR	P52721 thermarces
13	52	100.0	60	1	MTB_ONCMY	P09862 oncorhynch
14	52	100.0	60	1	MTB_SALSA	P52720 salmo salar
15	52	100.0	60	1	MT_AMBRE	O42152 amyristoma
16	52	100.0	60	1	MT_BRARE	P527122 brachydanio
17	52	100.0	60	1	MT_CARAU	P527123 carassius a
18	52	100.0	60	1	MT_CHAAC	P52724 chaenoceph
19	52	100.0	60	1	MT_CYPQA	O13369 cyprinus ca
20	52	100.0	60	1	MT_DICIA	O9P69g dicentrarch
21	52	100.0	60	1	MT_ESOLU	P25127 esox lucius
22	52	100.0	60	1	MT_GADMO	P51902 gadus morhu
23	52	100.0	60	1	MT_ICTFU	O93371 ictalurus p
24	52	100.0	60	1	MT_LITAU	O13357 litia aurata
25	52	100.0	60	1	MT_NOEBA	P25128 noemacheili
26	52	100.0	60	1	MT_OREMO	P52726 oreochromis
27	52	100.0	60	1	MT_PAGRE	O92145 pagothenia
28	52	100.0	60	1	MT_PARCR	O93450 paracheanic
29	52	100.0	60	1	MT_PERLU	P52725 perca fluvi
30	52	100.0	60	1	MT_PLEPL	P07216 pleuroctete
31	52	100.0	60	1	MT_PSELM	P55345 pseudopleur
32	52	100.0	60	1	MT_RUTRU	P80593 rutilus rut
33	52	100.0	60	1	MT_ZOAVI	P52728 zoarces viv

34	52	100.0	61	1	MTJA_BOVIN	P043560	bos	taurus
35	52	100.0	61	1	MTJA_HORSE	P028800	equus	cabala
36	52	100.0	61	1	MTJA_HUMAN	P047231	homo	sapiens
37	52	100.0	61	1	MTJA_RABBIT	P11957	homo	sapiens
38	52	100.0	61	1	MTJB_HORSE	P02801	equus	cabala
39	52	100.0	61	1	MTJB_HUMAN	P07438	homo	sapiens
40	52	100.0	61	1	MTJB_SHEEP	P05577	ovis	aries
41	52	100.0	61	1	MTJC_SHEEP	P05578	ovis	aries
42	52	100.0	61	1	MTJE_HUMAN	P04723	homo	sapiens
43	52	100.0	61	1	MTJG_HUMAN	P13640	homo	sapiens
44	52	100.0	61	1	MTJH_HUMAN	P35942	bos	taurus
45	52	100.0	61	1	MTJH_BOVIN			

ALIGNMENTS

RESULT	ID	MTA.COLVI	STANDARD:	PRF:	43 AA.
AC	DT	01-AUG-1992 (rel. 23, created)			
DT	DT	01-AUG-1992 (rel. 23, last sequence update)			
DT	DT	01-NOV-1997 (rel. 35, last annotation update)			
DE	DT	METALLOTHIONEIN A (MTA) (FRAGMENT).			
OC	DT	Colinus virginianus (Bobwhite quail) (Common bobwhite).			
OC	DT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	DT	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;			
OC	DT	Odonotophorinae; Colinus.			
RN	DT	SEQUENCE FROM N.A.			
RP	DT	TISSUE=LIVER;			
RC	DT	MEDLINE=93247066; PubMed=8483164;			
RX	DT	Shatzker Z. L., Kage K., Sobieski R. J., Andrews G. K.;			
RA	DT	"Evolution of avian metallothionein: DNA sequence analyses of the			
RT	DT	turkey metallothionein gene and metallothionein cDNAs from pheasant			
RT	DT	and quail."			
RL	DT	J. Mol. Evol. 36:255-262(1993).			
CC	DT	-1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE			
CC	DT	RESIDUES THAT BIND VARIOUS HEAVY METALS.			
CC	DT	-1- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:			
CC	DT	FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA			
CC	DT	DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11			
CC	DT	CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE			
CC	DT	BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.			
CC	DT	-1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.			
CC	DT	-----			
CC	DT	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	DT	between the Swiss Institute of Bioinformatics and the EMBL outstation			
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CC	DT	use by non-profit institutions as long as its content is in no way			
CC	DT	modified and this statement is not removed. Usage by and for commercial			
CC	DT	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	DT	or send an email to license@isb-sib.ch).			
CC	DT	-----			
CC	DT	EMBL: X62511, CAA44370.1; -.			
DR	DR	PIR: S18173; S18173.			
DR	DR	PIR: S33378; S33378.			
DR	DR	PIR: S33380; S33380.			
DR	DR	PIR: S33382; S33382.			
DR	DR	HSSP: P04355; 2MRT.			
DR	DR	INTERPRO: IPR000006; -.			
DR	DR	INTERPRO: IPR003019; -.			
DR	DR	PFAM: PF00131; metalthio; 1.			
DR	DR	PROSITE: PS00203; METALLOTHIONEIN_VRT; PARTIAL.			
KW	DR	Metal-binding; Metal-thiolate cluster; Chelation.			
FT	FT	NON_TER	1	16	BETA.
FT	FT	DOMAIN	<1	1	
FT	FT	DOMAIN	17	>43	ALPHA.
FT	FT	METAL	2	2	CLUSTER B.
FT	FT	METAL	6	6	CLUSTER B.
FT	FT	METAL	8	8	CLUSTER B.
FT	FT	METAL	11	11	CLUSTER B.

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FT METAL 13 13 CLUSTER B.
FT METAL 16 16 CLUSTER B.
FT METAL 20 20 CLUSTER A.
FT METAL 21 21 CLUSTER A.
FT METAL 23 23 CLUSTER A.
FT METAL 24 24 CLUSTER A.
FT METAL 28 28 CLUSTER A.
FT METAL 31 31 CLUSTER A.
FT METAL 35 35 CLUSTER A.
FT METAL 37 37 CLUSTER A.
FT NON_TER 43 43
SQ SEQUENCE 43 AA: 4401 MW: 1612EB52656EB875 CRC64:

Query Match 100.0%; Score 52; DB 1; Length 43;
Best Local Similarity 20.0%; Pred. No. 43;
Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXCXXXXXXXXXXCXXC 20
DB 16 CRKSCSCCPACGNNCAKGC 35

RESULT 2
MTB_COLVI STANDARD: PRT: 43 AA.
AC P27087.
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN B (MTB) (FRAGMENT).
OS Colinus virginianus (Bobwhite quail) (Common bobwhite).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Odontophorinae; Colinus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=93247066; PubMed=8483164;
RA Shatzker R.L., Kage K., Sobleski R.J., Andrews G.K.;
RT "Evolution of avian metallothionein: DNA sequence analyses of the
RT turkey metallothionein gene and metallothionein cDNAs from pheasant
RT and quail."
RL J. Mol. Evol. 36:255-262(1993).
CC -I- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS.
CC -I- DOMAIN: CLASS 1 METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11
CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
CC BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X62512; CAA44371.1; -.
DR PIR: S18174; S18174.
DR PIR: S33379; S33379.
DR HSSP: P04355; 2MRT.
DR INTERPRO: IPR000006; -.
DR INTERPRO: IPR003019; -.
DR PFAM: PF00131; metalthio; 1.
DR PROSITE: PS00203; METALLOTHIONEIN_VRT; PARTIAL.
KW Metal-binding; Metal-thiolate cluster; Chelation.
FT NON_TER 1 16 BETA
FT DOMAIN <1 16
FT DOMAIN 17 >43 ALPHA.
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FT METAL 2 2 CLUSTER B.
FT METAL 6 6 CLUSTER B.
FT METAL 8 8 CLUSTER B.
FT METAL 11 11 CLUSTER B.
FT METAL 13 13 CLUSTER B.
FT METAL 16 16 CLUSTER B.
FT METAL 20 20 CLUSTER A.
FT METAL 21 21 CLUSTER A.
FT METAL 23 23 CLUSTER A.
FT METAL 24 24 CLUSTER A.
FT METAL 28 28 CLUSTER A.
FT METAL 31 31 CLUSTER A.
FT METAL 35 35 CLUSTER A.
FT METAL 37 37 CLUSTER A.
FT NON_TER 43 43
SQ SEQUENCE 43 AA: 4429 MW: 1612EB40EE6EB875 CRC64:

Query Match 100.0%; Score 52; DB 1; Length 43;
Best Local Similarity 20.0%; Pred. No. 43;
Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXCXXXXXXXXXXCXXC 20
DB 16 CRKSCSCCPACGNNCAKGC 35

RESULT 3
THN_PVRPU STANDARD: PRT: 47 AA.
AC P07504.
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DE 01-JUL-1993 (Rel. 26, Last annotation update)
DE THIONIN.
GN TH1.
OS Pyricularia pubera (Rabbitwood) (Buffalo nut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Santalales; Santalaceae;
OC Pyricularia.
RN [1]
RP SEQUENCE.
RX MEDLINE=85173323; PubMed=3985614;
RA Vernon L.P., Eveitt G.E., Zeikus R.D., Gray W.R.;
RT "A toxic thionin from Pyricularia pubera: purification, properties, and
RT amino acid sequence."
RL Arch. Biochem. Biophys. 238:18-29(1985).
CC -I- FUNCTION: THIONINS ARE SMALL PLANT PROTEINS WHICH ARE TOXIC
CC TO ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE
CC LEVEL OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS,
CC OF THESE PROTEINS IS NOT KNOWN.
CC -I- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
CC -----
CC PIR: A24074; A24074.
DR HSSP: P01544; 2PLH.
DR MENDEL: 13438; PYRPU:TH1.3.
DR INTERPRO: IPR001010; -.
DR PFAM: PF00321; plant_thionins; 1.
DR PROSITE: PS00287; THIONIN.
DR PROSITE: PS00271; THIONIN; 1.
KW Thionin; Plant toxin.
FT DISULFID 3 41 BY SIMILARITY.
FT DISULFID 4 31 BY SIMILARITY.
FT DISULFID 16 27 BY SIMILARITY.
SQ SEQUENCE 47 AA: 5288 MW: 87E10460D8E4C6E1 CRC64:

Query Match 100.0%; Score 52; DB 1; Length 47;
Best Local Similarity 20.0%; Pred. No. 45;
Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXCXXXXXXXXXXCXXC 20
DB 12 CYNVCRLPPTTSRETCARKC 31
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Q	SEQUENCE	48 AA;	5101 MW;	0331C2D807F32FDC CRC64;
Q	SEQUENCE	48 AA;	5101 MW;	0331C2D807F32FDC CRC64;
FT	DISULFID	30	47	BY SIMILARITY.
FT	DISULFID	26	45	BY SIMILARITY.
FT	DISULFID	21	41	BY SIMILARITY.
FT	DISULFID	8	19	BY SIMILARITY.
FT	DISULFID	3	14	BY SIMILARITY.
FT	ACT SITE	27	28	REACTIVE BOND.
KW	Serine protease inhibitor.			
CC	-1- SIMILARITY: BELONGS TO THE ANTISTASIN FAMILY.			
CC	BE INVOLVED IN LEECH HEMATOPHAGIA.			
CC	-1- FUNCTION: INHIBITS PLASMA AND TISSUE KALLIKREIN, AND TRYPSIN.			
RL	Eur. J. Biochem. 254:692-697(1998).			
RT	"Amino acid sequence of piguamerin, an antistasin-type protease inhibitor from the blood sucking leech Hirudo nipponia.";			
RT	Kim D.R., Kang K.W.;			
RA	MEDLINE=98351570; Pubmed=9686284;			
RX	SEQUENCE.			
RN	[1]			
OC	Aynchobellida; Hirudiniiformes; Hirudiniidae; Hirudo.			
OC	Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;			
DE	PIGUAMERIN.			
OS	Hirudo nipponia.			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
AC	P81499;			
ID	PIGU_HIRNI	STANDARD;	PRT;	48 AA.
AC	P81499;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			

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Query Match          100.0%; Score 52; DB 1; Length 48;
Best Local Similarity 20.0%; Pred. No. 46;
Matches      4; Conservative 16; Mismatches      0; Indels      0; Caps      0
OY      1 CXXXCXXXXXXXXXXCXXC 20
         |:::|:::|:::|:::|:::|
Db      26 CRKCCPNNGFKKDEMGCTFPC 45

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RESULT	5
TX26_PHONI	
ID	TX26_PHONI
AC	STANDARD; PRT; 48 AA.
DT	P29425;
DT	01-APR-1993 (Rel. 25, Created)
DT	01-APR-1993 (Rel. 25, Last sequence update)
DT	01-APR-1993 (Rel. 25, Last annotation update)
DE	NEUROTOXIN TX2-6.
OS	Phonetrulia nigriverter (Brazilian armed spider).
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC	Araneomorphae; Entelegynae; Lycosoidae; Ctenidae; Phonetrulia.
RN	[1]
RP	SEQUENCE.
RC	TISSUE=VENOM;
RX	MEDLINE=93011905; PubMed=1397265;
RA	Cordeiro M.N., Diniz C.R., Valentim A.C., von Eickstedt V.R.D.,
RA	Gillroy J., Richardson M.;
RT	"The purification and amino acid sequences of four Tx2 neurotoxins
RT	from the venom of the Brazilian 'armed' spider Phonetrulia nigriverter
RT	(keys).";
RL	FEB8 Lett. 310:153-156(1992).
RL	FEBS Lett. 310:153-156(1992).
CC	-1- FUNCTION: CAUSES SCRATCHING, LACRIMATION, HYPERSALIVATION OF
CC	SWEATING AND AGITATION FOLLOWED BY SPASTIC PARALYSIS OF THE
CC	ANTERIOR AND POSTERIOR EXTREMITIES AND DEATH AT DOSE LEVELS OF
CC	0.79 MG/MOUSE. IT SIGNIFICANTLY ACTIVATES VOLTAGE-DEPENDENT SODIUM
CC	CHANNELS. INSECTICIDAL TO THE LARVAL AND ADULT FORMS OF THE HOUSE
CC	FLY.
CC	-1- SIMILARITY: TO NEUROTOXINS TX2-1 AND TX2-5.
DR	VENOM; Neurotoxin.
DR	PIR; S29216; S29216.
Q0	SEQUENCE 48 AA; 5298 MW; 4F30EBFCE9A19CD CRC64;

Query Match	100.0%	Score 52	DB 1	Length 48
Best Local Similarity	20.0%	Pred. No. 46		
Matches	4	Conservative 16	Mismatches 0	Indels 0
0y	1	CXXXCXXXXXXXXXXCXXC	20	
		::: ::: ::: ::: ::: :::		
Db	10	CKETDCCGEGECVCGGSPC	29	

RESULT	6	TX25_PHONE1	STANDARD:	PRT:	49 AA.
ID	TX25_PHONE1				
AC	P29424;				
DT	01-APR-1993 (Rel. 25, Created)				
DT	01-APR-1993 (Rel. 25, Last sequence update)				
DT	01-JUL-1993 (Rel. 26, Last annotation update)				
DE	NEUROTOXIN TX2-5.				
OS	Phonotritia nigriverter (Brazilian armed spider).				
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;				
OC	Araneomorphae; Entelegynae; Lycosoidae; Ctenidae; Phonotritia.				
NC	[1]				
RP	SEQUENCE.				
RC	TISSUE=VENOM:				
RX	MEDLINE=93011905; Pubmed=1397265.				
RA	Cordeiro M.N., Diniz C.R., Valentim A.C., von Elckstedt V.R.D.,				
RA	Gilroy J., Richardson M.;				
RT	"The purification and amino acid sequences of four Tx2 neurotoxins				
RT	"from the venom of the Brazilian 'armed' spider Phonotritia nigriverter				
RT	(keys)".;				
RL	FEBS Lett. 310:153-156(1992).				
RL	[2]				
RP	SEQUENCE OF 1-10.				
RC	TISSUE=VENOM:				
RX	MEDLINE=92196803; Pubmed=1801316;				
RA	Rezende L. Jr., Cordeiro M.N., Oliveira E.B., Diniz C.R.;				
RT	"Isolation of neurotoxic peptides from the venom of the 'armed'				
RT	spider Phonotritia nigriverter".;				
RL	Toxicol 29:1225-1233(1991).				
CC	-1- FUNCTION: CAUSES SCRATCHING, LACRIMATION, HYPERSALIVATION,				
CC	SWEATING AND AGITATION FOLLOWED BY SPASTIC PARALYSIS OF THE				
CC	ANTERIOR AND POSTERIOR EXTREMITIES AND DEATH AT DOSE LEVELS OF				
CC	0.24 MG/MOUSE. INSECTICIDAL TO THE LARVAL AND ADULT FORMS OF THE				
CC	HOUSE FLY.				
CC	-1- SIMILARITY: TO NEUROTOXINS TX2-1 AND TX2-6.				
DR	PIR: B39305; B39305.				
DR	PIR: S29215; S29215.				
DR	Venom; Neurotoxin.				
QO	SEQUENCE 49 AA: 5111 MW: 77846AAB3911716 CRC64;				

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Query Match          100.0%; Score 52; DB 1; Length 49;
Best Local Similarity 20.0%; Pred. No. 46;
Matches      4; Conservative 16; Mismatches      0; Indels      0; Gaps      0;

QY      1 CXXXCXXXXXXXXXXCXXXC 20
         |:::|:::|:::|:::|:::|
Db       10 CKVTCDCGGERGECVCGGPG 29

RESULT 7
ANTA_HIRME
ID ANTA_HIRME STANDARD; PRT; 55 AA.
AC P80302;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HIRUSTASTN.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinata; Hirudinea;
OC Aynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
NN [1]

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GN MST(3)Gt-9 OR MST87F.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN-CANTON-S;
 RX MEDLINE=88211557; PubMed=2835228;
 RA Kuhn R., Schaefer U., Schaefer M.;
 RT "Cis-acting regions sufficient for spermatocyte-specific
 RT transcriptional and spermatid-specific translational control of the
 RT Drosophila melanogaster gene mst(3)91-9.";
 RN EMBO J. 7:447-454(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aguayo A., An H.-J., Andrews-Plankoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Paulis B., Delcher A., Deng Z., Mays A.D., Dew I., Dletz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Flatschmann W.,
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleib J.M.,
 RA Palazkzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -1- TISSUE SPECIFICITY: TESTIS.
 CC -1- DEVELOPMENTAL STAGE: PRIMARY SPERMATOCYTES.
 CC -1- DOMAIN: THIS PROTEIN IS MOSTLY COMPOSED OF REPETITIVE C-G-P
 CC MOTIFS.
 CC -1- SIMILARITY: BELONGS TO THE MST(3)CGP FAMILY.
 CC -----
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 CC -----
 CC EMBL: Y00831; CAA68761.1; -.
 CC DR EMBL: AE003702; AMF54994.1; -.
 CC DR PIR: S00340; WTFP.

DR HSSP: P01180; INPO.
 DR FLYBASE: FBgn0002862; Mst87F.
 KW Spermatogenesis; Repeat; Multigene family.
 SQ SEQUENCE 56 AA; 5233 MW; 830CD131212C34A47 CRC64;
 Query Match 100.0%; Score 52; DB 1; Length 56;
 Best Local Similarity 20.0%; Pred. No. 51;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CXXXKXXXXXXXXXXCXXC 20
 DB 2 CCGPCGPGCGPCGCGPCG 21
 RESULT 10
 ID GUAM_HIRNT STANDARD; PRT; 57 AA.
 AC P46443;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GUAMERIN.
 OS Hirudo nipponia.
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudiniida; Hirudinea;
 OC Arynchobdellida; Hirudiformes; Hirudiniidae; Hirudo.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95293987; PubMed=7775446;
 RA Jung H.I., Kim S.I., Ha K.S., Joe C.O., Kang K.W.;
 RT "Isolation and characterization of guamerin, a new human leukocyte
 RT elastase inhibitor from Hirudo nipponia";
 RL J. Biol. Chem. 270:13879-13884(1995).
 CC -1- FUNCTION: INHIBITS MAMMALIAN ELASTASES.
 CC -1- TISSUE SPECIFICITY: NOT FOUND IN THE SALIVA, BUT IN THE BODY
 CC TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE ANTISTASIN FAMILY.
 CC DR HSSP: P80302; IHIA.
 DR Serine protease inhibitor.
 FT ACT SITE 36 37 REACTIVE BOND.
 FT DISULFID 12 23 BY SIMILARITY.
 FT DISULFID 17 28 BY SIMILARITY.
 FT DISULFID 30 50 BY SIMILARITY.
 FT DISULFID 35 54 BY SIMILARITY.
 FT DISULFID 39 56 BY SIMILARITY.
 SQ SEQUENCE 57 AA; 6123 MW; C5118B6E5481D7B CRC64;
 Query Match 100.0%; Score 52; DB 1; Length 57;
 Best Local Similarity 20.0%; Pred. No. 51;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CXXXKXXXXXXXXXXCXXC 20
 DB 35 CMIFCPNGKGVDENGCEYPC 54
 RESULT 11
 ID MTA_SPAU STANDARD; PRT; 60 AA.
 AC P52727;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE METALLOTHIONEIN A (MT A).
 GN MTA.
 OS Sparus aurata (Gilthead sea bream).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
 OC Sparidae; Sparus.
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;
RA Kille P., Olsson P.E.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Tom M.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Cousinou M., Lopez-Barea J., Dorado G.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
RESIDUES THAT BIND VARIOUS HEAVY METALS (BY SIMILARITY).
CC -I- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11
CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
CC -I- SIMILARITY: BELONGS TO FAMILY I IN METALLOTHIONEIN SUPERFAMILY.

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DR EMBL: X97276; CAA65931.1; -;
DR EMBL: U58774; AAC32738.1; -;
DR EMBL: U93206; AAB51590.1; -;
DR HSSP: P18055; IMRB.
DR INTERPRO: IPR000006; -;
DR INTERPRO: IPR003019; -;
DR PFM: PF00131; metalthio; 1.
DR PRINTS: PRO0860; MTEVERTEBRATE.
DR PROSITE: PS00203; METALLOTHIONEIN_VRT; 1.
KW Metal-binding; Metal-thiolate cluster; Chelation.
FT DOMAIN 1
FT DOMAIN 28
FT ALPHA. 29 60
FT METAL 4 4 CLUSTER B.
FT METAL 6 6 CLUSTER B.
FT METAL 12 12 CLUSTER B.
FT METAL 14 14 CLUSTER B.
FT METAL 18 18 CLUSTER B.
FT METAL 20 20 CLUSTER B.
FT METAL 23 23 CLUSTER B.
FT METAL 25 25 CLUSTER B.
FT METAL 28 28 CLUSTER B.
FT METAL 32 32 CLUSTER A.
FT METAL 33 33 CLUSTER A.
FT METAL 35 35 CLUSTER A.
FT METAL 36 36 CLUSTER A.
FT METAL 40 40 CLUSTER A.
FT METAL 43 43 CLUSTER A.
FT METAL 47 47 CLUSTER A.
FT METAL 49 49 CLUSTER A.
FT METAL 54 54 CLUSTER A.
FT METAL 58 58 CLUSTER A.
FT METAL 59 59 CLUSTER A.
SC SEQUENCE 60 AA; 5966 MW; 6A66F79D02BC591B CRC64;

RESULT	12
META_THEOR	ID META_THEOR STANDARD: PRT: 60 AA.
AC	P52721:
DT	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	01-NOV-1997 (Rel. 35, Last annotation update)
DE	METALLOTHIONEIN A (MT-A).
GN	MTA.
OS	Thermarces cerberus.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC	Acanthomorphi; Acanthopterygii; Percomorpha; Perciformes; Zoarcoidei;
OC	Zoarcidae; Thermarces.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=LIVER;
RA	Kille P., Olsson P.E.;
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC	-I- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC	RESIDUES THAT BIND VARIOUS HEAVY METALS (BY SIMILARITY)
CC	-I- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
CC	FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
CC	DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11
CC	CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
CC	BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
CC	-I- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
CC	-----
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; X97277; CAA65932.1; -.
DR	HSSP; P18055; IMRB.
DR	INTERPRO; IPRO00006; -.
DR	INTERPRO; IPRO03019; -.
DR	PFAM; PF00131; metalthio; 1.
DR	PRINTS; PR00860; MTVERTEBRATE.
DR	PROSITE; PS00203; METALLOTHIONEIN_VRT; 1.
KW	Metal-binding; Metal-thiolate cluster; Chelation.
FT	DOMAIN 1 28
FT	METAL 29 60
FT	METAL 4 4
FT	METAL 6 6
FT	METAL 12 12
FT	METAL 14 14
FT	METAL 18 18
FT	METAL 20 20
FT	METAL 23 23
FT	METAL 25 25
FT	METAL 28 28
FT	METAL 32 32
FT	METAL 33 33
FT	METAL 35 35
FT	METAL 36 36
FT	METAL 40 40
FT	METAL 43 43
FT	METAL 47 47
FT	METAL 49 49
FT	METAL 54 54
FT	METAL 58 58
FT	METAL 59 59
SE	SEQUENCE 60 AA: 6119 MW: F5C05DFB14F8821 CRC64;

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QY      1 CXXXXXXXXXXXXXXCXXC 20
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Db     28 CKKSCCSCCPAGCSKASGC 47
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Query Match	100.0%;	Score 52;	DB 1;	Length 60;
Best Local Similarity	20.0%;	Pred. No. 53;		
Matches	4;	Conservative 16;	Mismatches 0;	Indels 0;
			Gaps	0;

QY 1 CXXXXXXXXXXXXXXC 20
 ID P09862; STANDARD; PRT; 60 AA.
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE METALLOTHIONEIN B (MT-B).
 GN MTB.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri), and
 OS Salvelinus alpinus (Arctic char).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=O.MYKISS; PubMed=2448099;
 RX MEDLINE=88111026; PubMed=2448099;
 RA Bonham K., Zafarullah M., Gedamu L.;
 RT "The rainbow trout metallothioneins: molecular cloning and
 RL DNA 6:519-528(1987)."
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=O.MYKISS; PubMed=3185557;
 RX MEDLINE=89039876; PubMed=3185557;
 RA Zafarullah M., Bonham K., Gedamu L.;
 RT "Structure of the rainbow trout metallothionein B gene and
 RL Mol. Cell. Biol. 8:4469-4476(1988)."
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=O.MYKISS; TISSUE=LIVER;
 RX MEDLINE=91316146; PubMed=1859844;
 RA Kille P., Stephens P.E., Kay J.;
 RT "Elucidation of cDNA sequences for metallothioneins from rainbow
 RT trout, stone loach and pike liver using the polymerase chain
 RT reaction.";
 RL Biochim. Biophys. Acta 1089:407-410(1991)."
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.ALPINUS; TISSUE=LIVER;
 RA Gerpe M., Kling P., Olsson P.E.;
 RT "Metallothionein cDNA sequences and gene expression in arctic char
 RT (Salvelinus alpinus) following metal and PCB exposure.";
 RL Mar. Environ. Res. 46:551-554(1998)."
 CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
 CC RESIDUES THAT BIND VARIOUS HEAVY METALS (BY SIMILARITY).
 CC -1- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
 CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
 CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11
 CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
 CC BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
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 CC -----
 CC EMBL: M18104; AAA49566.1; -
 CC EMBL: M22487; AAA49567.1; -
 CC EMBL: X59394; CAA42037.1; -
 CC EMBL: AF013801; AAB6643.1; -

DR PIR; A30818; A30818.
 DR PIR; B27490; B27490.
 DR PIR; S16997; S16997.
 DR PIR; S15509; S15509.
 DR HSSP; P04355; 2MRT.
 DR INTERPRO; IPR000006; -
 DR INTERPRO; IPR003019; -
 DR PFAM; PF00131; metalthio. 1.
 DR PRINTS; PR00860; METALLOTHIONEIN VRT; 1.
 DR PROSITE; PS00203; METALLOTHIONEIN VRT; 1.
 KW Metal-binding; Metal-thiolate cluster; Chelation.
 FT DOMAIN 1 28
 FT 29 60
 FT METAL 4 4
 FT METAL 6 6
 FT METAL 12 12
 FT METAL 14 14
 FT METAL 18 18
 FT METAL 20 20
 FT METAL 23 23
 FT METAL 25 25
 FT METAL 28 28
 FT METAL 32 32
 FT METAL 33 33
 FT METAL 35 35
 FT METAL 36 36
 FT METAL 40 40
 FT METAL 43 43
 FT METAL 47 47
 FT METAL 49 49
 FT METAL 54 54
 FT METAL 58 58
 FT METAL 59 59
 SQ SEQUENCE 60 AA; 6033 MW; 9EA1E70FBE59B4EE CRC64;
 Query Match 100.0%; Score 52; DB 1; Length 60;
 Best local Similarity 20.0%; Pred. No. 53;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CXXXXXXXXXXXXXXC 20
 ID P52720; STANDARD; PRT; 60 AA.
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE METALLOTHIONEIN B (MT-B).
 GN MTB.
 OS Salmo salar (Atlantic salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Kille P., Olsson P.E.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
 CC RESIDUES THAT BIND VARIOUS HEAVY METALS (BY SIMILARITY).
 CC -1- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
 CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
 CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11
 CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
 CC BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
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CC or send an email to license@isb-sib.ch)).
CC -----
CC EMBL: X97275; CAA65930.1; -
CC DR HSSP: P18055; 1MRB.
CC DR INTERPRO: IPR000006; -
CC DR INTERPRO: IPR003019; -
CC DR PFAM: PF00131; metalchio; 1.
CC DR PRINTS: PRO0860; MTEVERTERATE.
CC DR PROSITE: PS00203; METALLOTHIONEIN_VRT; 1.
CC KW Metal-binding; Metal-thiolate cluster; Chelation.
CC
CC FT DOMAIN 1 28 ALPHA.
CC FT METAL 29 60
CC FT METAL 4 4 CLUSTER B.
CC FT METAL 6 6 CLUSTER B.
CC FT METAL 12 12 CLUSTER B.
CC FT METAL 14 14 CLUSTER B.
CC FT METAL 18 18 CLUSTER B.
CC FT METAL 20 20 CLUSTER B.
CC FT METAL 23 23 CLUSTER B.
CC FT METAL 25 25 CLUSTER B.
CC FT METAL 28 28 CLUSTER B.
CC FT METAL 32 32 CLUSTER A.
CC FT METAL 33 33 CLUSTER A.
CC FT METAL 35 35 CLUSTER A.
CC FT METAL 36 36 CLUSTER A.
CC FT METAL 40 40 CLUSTER A.
CC FT METAL 43 43 CLUSTER A.
CC FT METAL 47 47 CLUSTER A.
CC FT METAL 49 49 CLUSTER A.
CC FT METAL 54 54 CLUSTER A.
CC FT METAL 58 58 CLUSTER A.
CC FT METAL 59 59 CLUSTER A.
CC SQ SEQUENCE 60 AA; 5959 MW; 187A9D0FBESBD967 CRC64;

Query Match 100.0%; Score 52; DB 1; Length 60;
Best Local Similarity 20.0%; Pred. No. 53;
Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXCXXXXXXCXXC 20
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DB 28 CKKSCCPCPCGCKACSC 47

RESULT 15
MT_AMBME STANDARD: PRT; 60 AA.
AC 042152;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE METALLOTHIONEIN (MT).
GN MT-A.
OS Ambystoma mexicanum (Axolotl).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomidae;
OC Ambystoma.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EMBRYO;
RA Sault-Jacques E., Guay J., Wirtanen L., Huard V., Stewart G.,
RA Seguin C.;
RT "Cloning of a complementary DNA encoding an Ambystoma mexicanum
RT metallothionein, AmMT-A, and expression of the gene during early
RT development."
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS.

CC -!- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
CC FOUR DIVERGENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO-11
CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
CC BETA DOMAIN, CAN LIGATE THREE DIVERGENT IONS TO 9 CYSTEINES.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
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CC -----
CC DR EMBL: AF008583; AAB71835.1; -
CC DR HSSP: P04355; 2MRP.
CC DR INTERPRO: IPR000006; -
CC DR INTERPRO: IPR003019; -
CC DR PFAM: PF00131; metalchio; 1.
CC DR PRINTS: PRO0860; MTEVERTERATE.
CC DR PROSITE: PS00203; METALLOTHIONEIN_VRT; 1.
CC KW Metal-binding; Metal-thiolate cluster; Chelation.
CC
CC FT DOMAIN 1 28 ALPHA.
CC FT METAL 29 60
CC FT METAL 3 3 CLUSTER B.
CC FT METAL 5 5 CLUSTER B.
CC FT METAL 11 11 CLUSTER B.
CC FT METAL 13 13 CLUSTER B.
CC FT METAL 17 17 CLUSTER B.
CC FT METAL 19 19 CLUSTER B.
CC FT METAL 22 22 CLUSTER B.
CC FT METAL 24 24 CLUSTER B.
CC FT METAL 27 27 CLUSTER B.
CC FT METAL 31 31 CLUSTER A.
CC FT METAL 32 32 CLUSTER A.
CC FT METAL 34 34 CLUSTER A.
CC FT METAL 35 35 CLUSTER A.
CC FT METAL 39 39 CLUSTER A.
CC FT METAL 42 42 CLUSTER A.
CC FT METAL 46 46 CLUSTER A.
CC FT METAL 48 48 CLUSTER A.
CC FT METAL 56 56 CLUSTER A.
CC FT METAL 58 58 CLUSTER A.
CC FT METAL 59 59 CLUSTER A.
CC SQ SEQUENCE 60 AA; 5979 MW; AB05FA9153953279 CRC64;

Query Match 100.0%; Score 52; DB 1; Length 60;
Best Local Similarity 20.0%; Pred. No. 53;
Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXCXXXXXXCXXC 20
I:::|:|:|:|:|:|:|:|:|:|
DB 27 CKKSCCPCPCGCKGCGC 46

Search completed: March 1, 2001, 16:26:03
Job time: 400 sec